

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/609,383B
Source: 1FW/6
Date Processed by STIC: 9/27/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

SERIAL NUMBER: 10/609,383B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 **Wrapped Nucleics**
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
 - 2 **Invalid Line Length** The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
 - 3 **Misaligned Amino**
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
 - 4 **Non-ASCII** The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
 - 5 **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
 - 6 **PatentIn 2.0**
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
 - 7 **Skipped Sequences**
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
 - 8 **Skipped Sequences**
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
 - 9 **Use of n's or Xaa's**
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
 - 10 **Invalid <213>**
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
 - 11 **Use of <220>** Sequence(s) missing the ~~<220>~~ "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
 - 12 **PatentIn 2.0**
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
 - 13 **Misuse of n/Xaa** "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFW16

RAW SEQUENCE LISTING

DATE: 09/27/2006

PATENT APPLICATION: US/10/609,383B

TIME: 15:13:28

Input Set : F:\synthetic.txt

Output Set: N:\CRF4\09272006\J609383B.raw

see pp 7-8, too

1 <110> APPLICANT: Feldmann, Richard J.; Connectron Holding, Inc.
 3 <120> TITLE OF INVENTION: Synthetic Connectron
 5 <130> FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
 C--> 7 <140> CURRENT APPLICATION NUMBER: US/10/609,383B
 C--> 7 <141> CURRENT FILING DATE: 2003-07-01 *incorrect format*
 8 <150> PRIOR APPLICATION NUMBER: US 60/393,558 and US 09/866,925
 10 <160> NUMBER OF SEQ ID NOS: 34
 12 <170> SOFTWARE: Proprietary
 15 <210> SEQ ID NO: 1
 17 <211> LENGTH: 217
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Saccharomyces cerevisiae complete genome.
 21 <220> FEATURE:
 22 <222> LOCATION: (12572)...(12788)
 23 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 36
 26 <400> SEQUENCE: 1
 27 gcactggtaa caggtggtaa tgaagaagta atttcctgac ttgttggtgt actggtaaca 60
 28 ggtggtaaat atgaagtaat ttctgactt gttgtgttac tggtaacagg tggtaatgaa 120
 29 gaagtaattt cctgacttgt tgttgcaactg gtaacagggtg gtaatgatga agtaatttcc 180
 30 tgacttggtt ttgtactggt aacagggtgt aatgatg 217
 33 <210> SEQ ID NO: 2
 35 <211> LENGTH: 236
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Saccharomyces cerevisiae complete genome.
 39 <220> FEATURE:
 40 <222> LOCATION: (12572)...(12807)
 41 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 39
 44 <400> SEQUENCE: 2
 45 gcactggtaa caggtggtaa tgaagaagta atttcctgac ttgttggtgt actggtaaca 60
 46 ggtggtaaat atgaagtaat ttctgactt gttgtgttac tggtaacagg tggtaatgaa 120
 47 gaagtaattt cctgacttgt tgttgcaactg gtaacagggtg gtaatgatga agtaatttcc 180
 48 tgacttggtt ttgtactggt aacagggtgt aatgatgaag cagtttctg gcttgt 236
 51 <210> SEQ ID NO: 3
 53 <211> LENGTH: 166
 54 <212> TYPE: DNA
 55 <213> ORGANISM: Saccharomyces cerevisiae complete genome.
 57 <220> FEATURE:
 58 <222> LOCATION: (24863)...(25028)
 59 <223> OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 112
 62 <400> SEQUENCE: 3
 63 aatcaccaaa gtctacatat tctgtcttcatt cattaccacc tgttaccagt gcaacaacaa 60
 64 gtcaggaaat tactttcttca ttaccacctg ttaccactac aaaaacgagc gaacaaacca 120
 65 ctttggttac cgtgacatcc tgcgaatctc atgtgtgcac tgaatc 166

Does Not Comply
 Corrected Diskette Needed
 list as <1507 60/393,558
 <1517 2002-07-05, followed by
 <1507 09/866,925
 <1517 2001-05-30
 on line below

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Input Set : F:\synthetic.txt

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68 <210> SEQ ID NO: 4
70 <211> LENGTH: 37
71 <212> TYPE: DNA
72 <213> ORGANISM: Escherichia coli K-12 MG1655 complete genome.
74 <220> FEATURE:
75 <222> LOCATION: (4626130)...(4626166)
76 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
4651a
79 <400> SEQUENCE: 4
80 tctgatgaca aacgccaaac tgcctgatgc gctacgc 37
83 <210> SEQ ID NO: 5
85 <211> LENGTH: 54
86 <212> TYPE: DNA
87 <213> ORGANISM: Escherichia coli K-12 MG1655 complete genome.
89 <220> FEATURE:
90 <222> LOCATION: (705150)...(705203)
91 <223> OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =
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94 <400> SEQUENCE: 5
95 tctgatgaca aacgccaaac tgcctgatgc gctacgctta tcaggcctac gcag 54
98 <210> SEQ ID NO: 6
100 <211> LENGTH: 36
101 <212> TYPE: DNA
102 <213> ORGANISM: Escherichia coli K-12 MG1655 complete genome.
104 <220> FEATURE:
105 <222> LOCATION: (757718)...(757753)
106 <223> OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =
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109 <400> SEQUENCE: 6
110 ttacgcctga tgcgctgcgc ttatcaggcc tacggg 36
113 <210> SEQ ID NO: 7
115 <211> LENGTH: 37
116 <212> TYPE: DNA
117 <213> ORGANISM: Escherichia coli K-12 MG1655 complete genome.
119 <220> FEATURE:
120 <222> LOCATION: (4626130)...(4626166)
121 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
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124 <400> SEQUENCE: 7
125 tctgatgaca aacgccaaac tgcctgatgc gctacgc 37
128 <210> SEQ ID NO: 8
130 <211> LENGTH: 54
131 <212> TYPE: DNA
132 <213> ORGANISM: Escherichia coli K-12 MG1655 complete genome.
134 <220> FEATURE:
135 <222> LOCATION: (698713)...(698766)
136 <223> OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =
809
139 <400> SEQUENCE: 8
140 tctgatgaca aacgccaaac tgcctgatgc gctacgctta tcaggcctac gcag 54
143 <210> SEQ ID NO: 9
145 <211> LENGTH: 36
146 <212> TYPE: DNA

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147 <213> ORGANISM: Escherichia coli K-12 MG1655 complete genome.

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149 <220> FEATURE:
150 <222> LOCATION: (757718)...(757753)
151 <223> OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =
975
154 <400> SEQUENCE: 9
155 ttacgcctga tgcgctgcgc ttatcaggcc tacggg 36
158 <210> SEQ ID NO: 10
160 <211> LENGTH: 16
161 <212> TYPE: DNA
162 <213> ORGANISM: Saccharomyces cerevisiae complete genome - problem.
164 <220> FEATURE:
165 <222> LOCATION: (221330)...(221345)
166 <223> OTHER INFORMATION: Chromosome = 2 Strand = positive ConnectronObjectNumber =
792a
169 <400> SEQUENCE: 10
170 tatatatatg tcaactg 16
173 <210> SEQ ID NO: 11
175 <211> LENGTH: 16
176 <212> TYPE: DNA
177 <213> ORGANISM: Saccharomyces cerevisiae complete genome - problem.
179 <220> FEATURE:
180 <222> LOCATION: (221346)...(221361)
181 <223> OTHER INFORMATION: Chromosome = 2 Strand = positive ConnectronObjectNumber =
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184 <400> SEQUENCE: 11
185 tattgcatgc tggatg 16
188 <210> SEQ ID NO: 12
190 <211> LENGTH: 539
191 <212> TYPE: DNA
192 <213> ORGANISM: Saccharomyces cerevisiae complete genome - problem.
194 <220> FEATURE:
195 <222> LOCATION: (448454)...(448992)
196 <223> OTHER INFORMATION: Chromosome = 5 Strand = positive ConnectronObjectNumber =
4749
199 <400> SEQUENCE: 12
200 tatatatatg tcaactgtatt gcatgctgga tgggtgtaga caaggccgta gggacatata 60
201 gcatctagga agtaaccttg tacgaaaata ggcaatattt cctgttttagg cgattgtgac 120
202 gcagatttta gtccaacgat ctagecgtcaa ggaatttttt tatagtggga cattgcacca 180
203 aggaagtaac ttgatacgtc gtgggtgaat ggggtctgttt tcttattcgg cggggtaata 240
204 catttttggg ggaagtttgt ctgtctgacg cgccatatgt aggtacgcca aaaagggctc 300
205 ctctacttcg aagcgcgagg tcgtatacct aataaggaaa tgtaatttat aactttttat 360
206 tatattggtc ttttcgagag cggaacgtag gtccatgttt aaagtatcca agagaatatc 420
207 cacgaagcgg ctgagcaacg aacagaatcc tggttctcct cgactaagca gatagttaag 480
208 atactgtgca ccatggaaat tgaaaacgaa agtacgtacc gactacttta tttttgcag 539
210 <210> SEQ ID NO: 13
212 <211> LENGTH: 158
213 <212> TYPE: DNA
214 <213> ORGANISM: Saccharomyces cerevisiae complete genome - problem.
216 <220> FEATURE:
217 <222> LOCATION: (24863)...(25028)
218 <223> OTHER INFORMATION: Chromosome = 5 Strand = negative ConnectronObjectNumber =
4824a
221 <400> SEQUENCE: 13

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222 tatatatatg tcactgtatt gcatgctgga tgggtgtaga caaggccgta gggacatata

60

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223 gcaccttagga agtaaccttg tacgaaaata ggcaatattt cctgtttagg cgattgtgac      120
224 gcagatttta gtccaacgat ctagcgtcaa ggaatttt      158
226 <210> SEQ ID NO: 14
228 <211> LENGTH: 134
229 <212> TYPE: DNA
230 <213> ORGANISM: Halobacterium sp. NRC-1 complete genome.
232 <220> FEATURE:
233 <222> LOCATION: (732401)...(732534)
234 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
6612
237 <400> SEQUENCE: 14
238 ttcacacag acgaggacga gcgcggccaa gtgggggatcg gcacactcat cgtgttcac      60
239 gcgatggtgc tggtcgccgc gatcgccgcc ggcgtcctca tcaacactgc cggtacctc      120
240 caatccaagg ggtc      134
243 <210> SEQ ID NO: 15
245 <211> LENGTH: 193
246 <212> TYPE: DNA
247 <213> ORGANISM: Halobacterium sp. NRC-1 complete genome.
249 <220> FEATURE:
250 <222> LOCATION: (733018)...(733209)
251 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
6644a
254 <400> SEQUENCE: 15
255 gacgagcgcg gtcaagtggg gatcggcaca ctcatcgtgt tcatcgcgat ggtgctggtc      60
256 gccgcgatcg ccgccggcgt cctcatcaac accgccggct acctccaatc caaggggctcg      120
257 gcaaccggtg aggaagcctc cgcacaggtc tccaaccgca tcaacatcgt ctccgcgtac      180
258 ggcaacgtca aca      193
261 <210> SEQ ID NO: 16
263 <211> LENGTH: 85
264 <212> TYPE: DNA
265 <213> ORGANISM: Halobacterium sp. NRC-1 complete genome.
267 <220> FEATURE:
268 <222> LOCATION: (773399)...(773483)
269 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
6852
272 <400> SEQUENCE: 16
273 gtgggggatcg gcacgtcat cgtgttcac gcgatggtgc tggtcgccgc gatcgccgcc      60
274 ggcgtcctca tcaacactgc cggt      85
277 <210> SEQ ID NO: 17
279 <211> LENGTH: 121
280 <212> TYPE: DNA
281 <213> ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
283 <220> FEATURE:
284 <222> LOCATION: (4832718)...(4832838)
285 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
53464
288 <400> SEQUENCE: 17
289 gccaacatcg aggcctcaa cagccgcacg gtgaacatcg gccagatcct cgaagtgatc      60
290 aaggcatct ccgagcagac caacctgctc gccctcaacg ccgccatcga agccgcgcgc      120
291 g      121
294 <210> SEQ ID NO: 18
296 <211> LENGTH: 194
297 <212> TYPE: DNA

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298 <213> ORGANISM: Pseudomonas aeruginosa PA01, complete genome.

300 <220> FEATURE:

301 <222> LOCATION: (4836528)...(4836720)

302 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =

53531

305 <400> SEQUENCE: 18

306 ggacggcaaa caggtggctg agcagacat cgcgcgatg aacgagcttt ccgagaagat 60

307 cagcgcctcc tgcgccaaca tcgaggccct caacagccgc acggtgaaca tcggccagat 120

308 cctcgaagtg atcaagggca tctccgagca gaccaacctg ctgcgccctca acgccgccat 180

309 cgaagccgcg cgcg 194

312 <210> SEQ ID NO: 19

314 <211> LENGTH: 169

315 <212> TYPE: DNA

316 <213> ORGANISM: Pseudomonas aeruginosa PA01, complete genome.

318 <220> FEATURE:

319 <222> LOCATION: (4838678)...(4838846)

320 <223> OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =

53549a

323 <400> SEQUENCE: 19

324 accatccgcg cgatgaacga gctttccgag aagatcagcg cctcctgcgc caacatcgag 60

325 gccctcaaca gccgcacggt gaacatcggc cagatcctcg aagtgatcaa gggcatctcc 120

326 gagcagacca acctgctcgc cctcaacgcc gccatcgaag ccgcgcgcg 169

329 <210> SEQ ID NO: 20

331 <211> LENGTH: 36

332 <212> TYPE: DNA

333 <213> ORGANISM: Sequence Recognized by Synthetic DNA Binding Protein.

335 <220> FEATURE:

338 <400> SEQUENCE: 20

339 tccccatgag catagatatg caggtaggcg gcaagt

342 <210> SEQ ID NO: 21

344 <211> LENGTH: 136

345 <212> TYPE: DNA

346 <213> ORGANISM: Vibrio cholerae chromosome I, complete chromosome.

348 <220> FEATURE:

349 <222> LOCATION: (952641)...(952777)

350 <223> OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =

607

353 <400> SEQUENCE: 21

354 tgtatatacc caaactactt ggagttgcag gtaggcggca agtgagttag tccccatgag 60

355 catagataga ctatgtgatt ggggtgaacg aacgtagcca acaccgctgc agcttcaagt 120

356 aggaagggta tacctt 136

359 <210> SEQ ID NO: 22

361 <211> LENGTH: 117

362 <212> TYPE: DNA

363 <213> ORGANISM: Vibrio cholerae chromosome I, complete chromosome.

365 <220> FEATURE:

366 <222> LOCATION: (1005810)...(1005926)

367 <223> OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber =

646

370 <400> SEQUENCE: 22

371 taccaaaact acttggagtt gcaggtaggc ggcaagagag tgaatcccca tcagcataga 60

372 cagactatgt gattggggtg aacgaacgta gccaataccg ctgcagcttc aagtagg 117

375 <210> SEQ ID NO: 23

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/609,383B

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Input Set : F:\synthetic.txt
Output Set: N:\CRF4\09272006\J609383B.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 27,28,29,30
Seq#:2; Line(s) 45,46,47,48
Seq#:3; Line(s) 63,64,65
Seq#:4; Line(s) 76,80
Seq#:5; Line(s) 95
Seq#:6; Line(s) 110
Seq#:7; Line(s) 121,125
Seq#:8; Line(s) 140
Seq#:9; Line(s) 155
Seq#:10; Line(s) 170
Seq#:12; Line(s) 200,201,202,203,204,205,206,207,208
Seq#:13; Line(s) 222,223,224
Seq#:14; Line(s) 238,239,240
Seq#:15; Line(s) 255,256,257,258
Seq#:16; Line(s) 273,274
Seq#:17; Line(s) 289,290,291
Seq#:18; Line(s) 306,307,308,309
Seq#:19; Line(s) 324,325,326
Seq#:20; Line(s) 339
Seq#:21; Line(s) 354,355,356
Seq#:22; Line(s) 371,372
Seq#:23; Line(s) 385
Seq#:24; Line(s) 400,401,402
Seq#:25; Line(s) 417,418
Seq#:26; Line(s) 425,431
Seq#:27; Line(s) 438,444
Seq#:28; Line(s) 459,460
Seq#:29; Line(s) 475,476,477
Seq#:30; Line(s) 489
Seq#:31; Line(s) 500
Seq#:32; Line(s) 511
Seq#:33; Line(s) 522
Seq#:34; Line(s) 533

VERIFICATION SUMMARY

DATE: 09/27/2006

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Output Set: N:\CRF4\09272006\J609383B.raw

L:7 M:270 C: Current Application Number differs, Missing <140> CURRENT APPLICATION NUMBER: is Added.

L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date